Amendments to the Claims:

1-25. (Withdrawn)

26. (Original) A method for evaluating user-supplied genomics data using a structured database that permits the computation of complex relationships among genes and/or gene products contained in the database, comprising:

(a) defining a profile model based on one or more profile definition criterion;

(b) building a collection of profiles according to the profile model;

(c) identifying one or more profiles that overlap at least a portion of the user-supplied genomics data and determining, for each such overlapped profile, whether the overlap is statistically significant; and

(d) analyzing one or more statistically significant profiles together with the user supplied genomics data including inspecting database-asserted biological interactions embodied in the one or more statistically significant profiles.

27. (Original) The method of claim 26, further including the step of pre-generating a profile library containing a profile for each one of a genomic information type in the database according to the profile model.

28. (Original) The method of claim 27, wherein the profiles are pre-generated from a graph structure.

29. (Original) The method of claim 26, further comprising the step of generating profiles by querying the database for information matching the one or more profile definition criterion.

30. (Original) The method of claim 28, wherein the determining statistical significance step includes the step of computing a probability of overlap as a function of information contained in the database.

31. (Original) The method of claim 26, wherein the genomic information type is one of a gene, gene product and biological process.

32. (Original) The method of claim 26, wherein the user-supplied genomics data is differential gene expression data and the analyzing step further includes one of the steps of:

(1) identifying a new use for a known therapy wherein the gene expression data relates to a pathway affected by the known therapy;

(2) prioritizing candidate development compounds for further development wherein the gene expression data relates to the target of one or more candidate development compounds and the analyzing step includes giving higher priority to development compounds on the basis of whether or not they are likely to result in an undesirable effect based on their involvement in other biological pathways as embodied in the profile; and

(3) identifying disease-related pathways wherein the disease is a side effect of drug therapy, wherein the gene expression data relates to the target affected by the drug therapy and the alternative pathways that are also affected by the drug or the drug discovery target and that result in an undesirable phenotype are embodied in the profile.

33. (Original) The method of claim 26, wherein the genomics data is differential gene expression data relating to particular disease, and wherein the analyzing step further includes the step of validating whether the gene expression data are genotypic markers for the disease state according to whether a database-asserted biological association related to the disease state, which is shared among a plurality of overlapped profiles, is statistically significant.

34. (Original) The method of claim 26, wherein the profile generation criterion include one or more of a biological process, number of genes, organismal, gene connectivity, edge connectivity, findings source type, experiment context, and tissue consistency criterion.

35. (Original) The method of claim 26, wherein the profiles are generated from a seed node and the inspecting database-asserted biological interactions step focuses on the biological interactions emanating from the seed node.

36. (Original) The method of claim 35, wherein the seed is one of a gene, gene product and biological process genomic data type.

37. (Original) The method of claim 26, further comprising computing a statistical significance for a biological association in the one or more statistically significant profiles.

38. (Original) The method of claim 26, wherein the generating a profile library step includes, for each profile generated, the step of selecting a node for a profile based on the number of similar findings in the database that link the node to a neighboring node.

39. (Original) The method of claim 26, further comprising the step of displaying information related to the one or more statistically significant profiles and genomics data using a GUI.

40. (Original) The method of claim 26, further including the step of annotating the profiles with biological associations asserted by the database including one or more of a cellular process, molecular process, organismal process and disease process.

41. (Original) The method of claim 40, further including the step of displaying biological association using one of a GUI and a report.

42. (Original) The method of claim 40, wherein the annotation of profiles includes using classification information found in an ontology.

43. (Original) The method of claim 26, wherein the determining of statistical significance test includes testing a null hypothesis over a discrete probability distribution, the distribution being a function of the database size, profile sizes, the user-supplied genomics data size and expression values.

44. (Original) The method of claim 26, wherein the generating step includes generating a plurality of profile libraries, each of which corresponding to a different one of a plurality of profile generation criterions.

45-53. (Withdrawn)